

Exhibit E

SEQ ID NO: 1 mapping to the human genome

MEGABLAST 1.2.3-Paracel [2001-11-20]

Reference:

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),

"A greedy algorithm for aligning DNA sequences",

J Comput Biol 2000; 7(1-2):203-14.

Database: Homo_sapiens.latestgp.masked.fa

33,840 sequences; 200,810,911,373 total letters

Query= LEX413bestorf
(1116 letters)

Sequences producing significant alignments:

	Score (bits)	E Value
AC013467.8.1.172966	866	0.0
AC104304.2.1.202933	<u>414</u>	e-113
AC098613.2.1.185437	<u>313</u>	1e-82

>AC013467.8.1.172966
Length = 172966

Score = 866 bits (437), Expect = 0.0
Identities = 820/943 (86%), Gaps = 28/943 (2%)
Strand = Plus / Minus

Query: 25 gacatttctgtcatcagagccttgtgggaaactcgtgtcaagaagcacaaagcttggcag 84
|||||
Sbjct: 169343 gacatttctgttgtcagagccttgtgggaaacttgtgtcaagaagcac-aagtttggcag 169285

Query: 85 aagaaggaggtggaaaggcttgagaagagcgccttggagaagataaaggaggagtggaaac 144
|||||
Sbjct: 169284 aagaaggaggcagaaagtcttgagaagagtgcacagaaaagacaaaggaggagtggccc 169225

Query: 145 tttgtggccgaa-tgcaggaggaagggcatccccaggctgta-tactg-caag-a-a-t 198
|||
Sbjct: 169224 cttgaggtc-aagtgcaggaggaagggcatctcctgggctg-agtactggctgggatagt 169167

Query: 199 ggcttcatagacac-ca--gcgtgcggcttctggacaagattgaaaggaaca-ctctcac 254
|||||
Sbjct: 169166 ggcttcatagacattcatagcatgcagcttctggaaaagatagaaaggaa-agctctcac 169108

Query: 255 aaggcagagttcacttcccaaggacagaggcaaacggagcagtgcgtttgtgtttgaact 314
|||||
Sbjct: 169107 aaggcagagttcacttcccaaggacagaggcaaataggagcagtggtttgtgtttggact 169048

Query: 315 ttctgggggagcactggacggagctcccagattcattgaaggagcagacacacctgagaga 374
 |||
 Sbjct: 169047 ttctgggggagtactggacggagctgccagatttgtaaaggagcagacgcacctgagaga 168988

```
Query: 435      gatgagaattctggatctgccaaa-aaaccaaattcacatcttccagcagaaa-tcggt 492
               ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 168927   gatgagaattcaggatctgccaaagaaac-aaatctcacattttccagct-aaactcagt 168870
```

```
Query: 553      gaattgggagattgtgaaaatctagagagactggattgttctggaaatctagaattaatg 612  
              ||   ||||||||| | ||||| | ||||| | ||||| | ||||| | ||||| |  
Sbjct: 168809 gagctgggagattgtgaaa-tctagagggaactggattgttctggaaatctggaattcaca 168751
```

Query: 673 aagttttccagtggtcccaatctgtgtcctgcggatgtcgaatttgcagtggttggaatc 732
|||||
Sbjct: 168690 aagttttccagtggtcccaatctgtgtcctgcggatgtcgaatttgcagtggttggaatc 168632

Query: 792 ctttctcttgataaaaaacaagttgacctaccttcctattccatgctgaacctgaagaa 851
 |||
 Sbjct: 168576 ctttctcttgatagaagcaagttgacctaccttcctaccccatgcttaacctgaagaa 168517

```
Query: 911      actcatccacacctttaaatttgtaagccttatggacaatcc 953  
          ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 168457 actcctccacacctttaaatttgtaagccttataaacatcc 168415
```

Identities = 81/86 (94%), Gaps = 2/86 (2%)
Strand = Plus / Minus

Query: 1032 tatgaaagcctatatattgaagaccttaagaaagagaatctgttccca-gctataccacca 1090
|||||
Sbjct: 167819 tatgaaagcctatatattgaagatcttaaggaaagagaatctgt-cccaagctataccacca 167761

Query: 1091 aagtgtcttttagccttcaactttga 1116
|||
Sbjct: 167760 aagggtcttttagccttcaactttga 167735

>AC104304.2.1.202933

Length = 202933

Score = 414 bits (209), Expect = e-113
Identities = 209/209 (100%)
Strand = Plus / Minus

Query: 126 gataaaggaggagtggaaactttgtggccgaatgcaggaggaagggcatccccaggctgt 185
|||||
Sbjct: 77595 gataaaggaggagtggaaactttgtggccgaatgcaggaggaagggcatccccaggctgt 77536

Query: 186 atactgcaagaatggcttcatagacaccagcgtgcggttctggacaagattgaaaggaa 245
|||||
Sbjct: 77535 atactgcaagaatggcttcatagacaccagcgtgcggttctggacaagattgaaaggaa 77476

Query: 246 cactctcacaaggcagagttcacttcccaaggacagaggcaaacggagcagtgcgtttgt 305
|||||
Sbjct: 77475 cactctcacaaggcagagttcacttcccaaggacagaggcaaacggagcagtgcgtttgt 77416

Query: 306 gtttgaactttctggggagcactggacgg 334
|||||
Sbjct: 77415 gtttgaactttctggggagcactggacgg 77387

Score = 317 bits (160), Expect = 8e-84
Identities = 160/160 (100%)
Strand = Plus / Minus

Query: 333 ggagctcccagattcattgaaggagcagacacacctgagagaatggtacataagcaatac 392
|||||
Sbjct: 71544 ggagctcccagattcattgaaggagcagacacacctgagagaatggtacataagcaatac 71485

Query: 393 cttgattcaaatacttcctacatatattcagttatttcaagcgatgagaattctggatct 452
|||||
Sbjct: 71484 cttgattcaaatacttcctacatatattcagttatttcaagcgatgagaattctggatct 71425

Query: 453 gccaaaaaaccaaatctcacatcttccagcagaaatcggt 492
|||||
Sbjct: 71424 gccaaaaaaccaaatctcacatcttccagcagaaatcggt 71385

Score = 313 bits (158), Expect = 1e-82
Identities = 158/158 (100%)
Strand = Plus / Minus

Query: 772 aggctagaggagctgcagagctttctcttgataaaaaacaagttgacctaccttcctat 831
|||||
Sbjct: 59926 aggctagaggagctgcagagctttctcttgataaaaaacaagttgacctaccttcctat 59867

Query: 832 tccatgctgaacctgaagaagctcactctgttagtcgtcagtgaggaccatttggtggag 891
|||||
Sbjct: 59866 tccatgctgaacctgaagaagctcactctgttagtcgtcagtgaggaccatttggtggag 59807

Query: 892 ctcccaactgccctttgtgactcatccacacctttaa 929
|||||
Sbjct: 59806 ctcccaactgccctttgtgactcatccacacctttaa 59769

Score = 291 bits (147), Expect = 5e-76
Identities = 147/147 (100%)
Strand = Plus / Minus

Query: 628 ttaagtaatttgaagcaagttacattttagatatctcagcaaacaagttttccagtgtc 687
|||||
Sbjct: 62392 ttaagtaatttgaagcaagttacattttagatatctcagcaaacaagttttccagtgtc 62333

Query: 688 ccaatctgtgtcctgcggatgtcgaatttgcagtggttgatatacagcagcaataacctg 747
|||||
Sbjct: 62332 ccaatctgtgtcctgcggatgtcgaatttgcagtggttgatatacagcagcaataacctg 62273

Query: 748 accgacctgccgcaagatatagacagg 774
|||||
Sbjct: 62272 accgacctgccgcaagatatagacagg 62246

Score = 276 bits (139), Expect = 3e-71
Identities = 142/143 (99%)
Strand = Plus / Minus

Query: 490 ggttggttgaagaacctgaaagaactcaatgtgggtttcaactatctgaagagcattcct 549
|||||

Sbjct: 65252 ggttggttgaagaacctgaaagaactcaatgtgggtttcaactatctgaagagcattcct 65193

Query: 550 ccagaattgggagattgtgaaaatctagagagactggattgttctggaaatctagaatta 609
|||||

Sbjct: 65192 ccagaattgggagattgtgaaaatctagagagactggattgttctggaaatctagaatta 65133

Query: 610 atggagctgccctttgaattaag 632
|||||

Sbjct: 65132 atggagctgccctttgaagtaag 65110

Score = 272 bits (137), Expect = 4e-70
Identities = 137/137 (100%)
Strand = Plus / Minus

Query: 930 atttgtaagccttatggacaatcctattgataatgcccaatgtgaagatggcaatgaaat 989
|||||

Sbjct: 53987 atttgtaagccttatggacaatcctattgataatgcccaatgtgaagatggcaatgaaat 53928

Query: 990 aatggaaagtgaacgggatcgccaacattttgataaagaagttatgaaagcctatattga 1049
|||||

Sbjct: 53927 aatggaaagtgaacgggatcgccaacattttgataaagaagttatgaaagcctatattga 53868

Query: 1050 agaccttaaagaaagag 1066
|||||

Sbjct: 53867 agaccttaaagaaagag 53851

Score = 250 bits (126), Expect = 2e-63
Identities = 126/126 (100%)
Strand = Plus / Minus

Query: 1 atgggacataaagtgggtgtcttcgacatttctgtcatcagagccttgtgggaaactcgt 60
|||||

Sbjct: 83933 atgggacataaagtgggtgtcttcgacatttctgtcatcagagccttgtgggaaactcgt 83874

Query: 61 gtcaagaagcaciaaagcttggcagaagaaggaggtggaaaggcttgagaagagcgccttg 120
|||||

Sbjct: 83873 gtcaagaagcaciaaagcttggcagaagaaggaggtggaaaggcttgagaagagcgccttg 83814

Query: 121 gagaag 126
|||||

Sbjct: 83813 gagaag 83808

Score = 103 bits (52), Expect = 2e-19

Identities = 52/52 (100%)
Strand = Plus / Minus

Query: 1065 agaatctgttcccagctataaccaccaaagtgtcttttagccttcaactttga 1116
|||||
Sbjct: 51394 agaatctgttcccagctataaccaccaaagtgtcttttagccttcaactttga 51343

>AC098613.2.1.185437
Length = 185437

Score = 313 bits (158), Expect = 1e-82
Identities = 158/158 (100%)
Strand = Plus / Minus

Query: 772 aggctagaggagctgcagagctttctcttgataaaaaacaagttgacctaccttcctat 831
|||||
Sbjct: 184111 aggctagaggagctgcagagctttctcttgataaaaaacaagttgacctaccttcctat 184052

Query: 832 tccatgctgaacctgaagaagctcactctgttagtcgtcagtgaggaccatttggtggag 891
|||||
Sbjct: 184051 tccatgctgaacctgaagaagctcactctgttagtcgtcagtgaggaccatttggtggag 183992

Query: 892 ctcccaactgccctttgtgactcatccacaccttttaa 929
|||||
Sbjct: 183991 ctcccaactgccctttgtgactcatccacaccttttaa 183954

Score = 272 bits (137), Expect = 4e-70
Identities = 137/137 (100%)
Strand = Plus / Minus

Query: 930 atttgtaagccttatggacaatcctattgataatgcccaatgtgaagatggcaatgaaat 989
|||||
Sbjct: 178186 atttgtaagccttatggacaatcctattgataatgcccaatgtgaagatggcaatgaaat 178127

Query: 990 aatggaaagtgaacgggatcgccaacattttgataaagaagttatgaaagcctatattga 1049
|||||
Sbjct: 178126 aatggaaagtgaacgggatcgccaacattttgataaagaagttatgaaagcctatattga 178067

Query: 1050 agaccttaaagaaagag 1066
|||||
Sbjct: 178066 agaccttaaagaaagag 178050

Score = 103 bits (52), Expect = 2e-19
Identities = 52/52 (100%)

Strand = Plus / Minus

Query: 1065 agaatctgttcccagctataaccaccaaagtgtcttttagccttcaactttga 1116
 ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 175593 agaatctgttcccagctataaccaccaaagtgtcttttagccttcaactttga 175542